

Serial No. 09/723,185

Page 2

II. Claims 27-44 and 46, drawn to peptides falling under the generic sequence of SEQ ID NO:32 (claim 31).

In the parent application, applicants elected group I for prosecution on the merits, and non-elected claims 27-44 and 46 were canceled. This application, however, covers a portion of Group II (claims 27-30). Hence, the above application is in fact a divisional application.

Attached is a Supplemental Application Data Sheet indicating the correction of the docket number in this case, to reflect that it is a divisional application (P1071P2C2 to P1071P2D1). Please note that only the docket no. is being changed on this application, not other application data. Applicants affirmatively request that the USPTO continue directing correspondence to the address of record.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned "Version with markings to show changes made."

For the Examiner's convenience, a clean copy of the currently pending claims is attached hereto.

If the Examiner has any questions, he should feel free to call the undersigned attorney at the number indicated below.

Respectfully submitted,
GENENTECH, INC.

Date: November 8, 2002

By: Janet E. Hasak
Janet E. Hasak
Reg. No. 28,616
Telephone No. (650) 225-1896



09157

PATENT TRADEMARK OFFICE

\\PFDesktop\1\ODMA\PCDOCS\GENENLAW\124213\1

Serial No. 09/723,185

Page 3

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Claims:

Claims 31-44 and 46 have been canceled.

@PFDesktop\1:ODMA/PCDOCS/GENENLAW/124213/1

Serial No. 09/723,185

Page 4

CLEAN SET OF PENDING CLAIMS

27. A constrained helical peptide comprising a sequence of nine amino acid residues having a first terminal residue and a second terminal residue, wherein said residues flank an internal sequence of seven amino acids and have side-chains covalently bonded to each other to form a locking moiety and thereby constrain the peptide.

28. The peptide of claim 27 wherein the internal sequence is Xaa(7)LeuAlaXaa(10)Xaa(11)Xaa(12)Xaa(13) (SEQ ID NO:31), wherein Xaa(7), Xaa(11), Xaa(12), and Xaa(13) are independently Nal(1), His, Phe, Trp, Tyr, Pro, Gln, or Met, and Xaa(10) is any amino acid.

29. The peptide of claim 28 wherein the first and second terminal residues are independently Asp or Glu residues.

30. The peptide of claim 29 wherein the first and second terminal residues are Glu residues.

52. The peptide of claim 28 wherein Xaa(7) is Trp.

53. The peptide of claim 28 wherein Xaa(10) is Glu.

54. The peptide of claim 28 wherein Xaa(11) is Lys.

55. The peptide of claim 28 wherein Xaa(12) is Tyr.

56. The peptide of claim 28 wherein Xaa(13) is Phe.

57. The peptide of claim 28 wherein Xaa(7) is Trp, Xaa(10) is Glu, Xaa(11) is Lys, Xaa(12) is Tyr, and Xaa(13) is Phe.

©PFDdesktop\.:ODMA/PCDOCS/GENENLAW/124213/1